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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/600,070	06/20/2003	Katherine W. Osteryoung	MSU-08153	5938

7590 03/03/2006

J. Mitchell Jones
MEDLEN & CARROLL, LLP
Suite 350
101 Howard Street
San Francisco, CA 94105

EXAMINER	
KUBELIK, ANNE R	
ART UNIT	**PAPER NUMBER**
1638	

DATE MAILED: 03/03/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/600,070	OSTERYOUNG ET AL.	
	Examiner	Art Unit	
	Anne R. Kubelik	1638	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *23 May 2005 and 17 August 2005*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1,4-6,8-17 and 22* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1,4-6,8-17 and 22* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *24 February 2004* is/are: a)☐ accepted or b)☒ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: *search results*.

DETAILED ACTION

1. Applicant's election without traverse of Group I (claims 1, 4-6, 8-17 and 22) in the reply filed on 23 May 2005 is acknowledged. Applicant also elects SEQ ID NO:3 and states that the remaining sequences will be examined if the elected sequences is found allowable. This is not true; the requirement to select a single sequence specifically states that this is a restriction, not an election of species. Furthermore, claim 1is not treated as a linking claim for the sequences, as all the sequences are recited in the alternative.

SEQ IS NO:3 is the genomic sequence encoding SEQ ID NO:2; SEQ ID NO:1 is the cDNA encoding SEQ ID NO:2. The claims will be examined to the extent they are drawn to nucleic acids encoding SEQ ID NO:2, and the restriction between SEQ ID NO:1 and 3 is withdrawn.

Applicant is required to cancel nonelected sequences or take other appropriate action (37 CFR 1.144). See MPEP § 821.01.

The requirement is still deemed proper and is therefore made FINAL.

2. The drawings filed 24 February 2004 are objected to for the following reasons:

Figures 1-2, 6-24 and 26-27 are objected to because tables and sequence listings that are included in the specification are, except for applications filed under 35 U.S.C. 371, are not permitted to be included in the drawings. See 37 CFR 1.83 (a).

Figures 5, 8-10, 12, 17, 20, 24, 26 are objected to because partial figures intended to form one complete view, on one or several sheets, must be identified by the same number followed by a capital letter. See 37 CFR 1.84 (u).

Figures 4-5 and 25 are objected to because the letters in the black boxes cannot be made out.

Corrected drawing sheets in compliance with 37 CFR 1.121(d) are required in reply to the Office action to avoid abandonment of the application. Any amended replacement drawing sheet should include all of the figures appearing on the immediate prior version of the sheet, even if only one figure is being amended. The figure or figure number of an amended drawing should not be labeled as "amended." If a drawing figure is to be canceled, the appropriate figure must be removed from the replacement sheet, and where necessary, the remaining figures must be renumbered and appropriate changes made to the brief description of the several views of the drawings for consistency. Additional replacement sheets may be necessary to show the renumbering of the remaining figures. Each drawing sheet submitted after the filing date of an application must be labeled in the top margin as either "Replacement Sheet" or "New Sheet" pursuant to 37 CFR 1.121(d). If the examiner does not accept the changes, the applicant will be notified and informed of any required corrective action in the next Office action. The objection to the drawings will not be held in abeyance.

3. The disclosure is objected to for the following reasons:

It contains embedded hyperlinks and/or other form of browser-executable code. See pg 40, line 29; pg 41, lines 1 and 3; pg 60, line 20; pg 86, line 26; pg 87, lines 4, 6, 9, 11, 13, 15, 16 and 19-30; pg 88, lines 2-3, 7-10, 14 and 17; pg 94, lines 3, 6-8; pg 103, lines 5 and 8; and pg 11, line 4. Applicant is required to delete the embedded hyperlinks and/or other form of browser-executable code. See MPEP § 608.01.

The Brief Description of Figure 5 is objected to because the symbols are missing.

4. It is suggested that Table 3 be amended to include the SEQ ID NOs: for each sequence.

Claim Objections

5. Applicant is advised that should claims 8-12 be found allowable, claims 13-17 will be objected to under 37 CFR 1.75 as being a substantial duplicate thereof. When two claims in an

application are duplicates or else are so close in content that they both cover the same thing, despite a slight difference in wording, it is proper after allowing one claim to object to the other as being a substantial duplicate of the allowed claim. See MPEP § 706.03(k).

Claim Rejections - 35 USC § 112

6. The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

7. Claims 1, 4-6 and 8-17 are rejected under 35 U.S.C. 112, first paragraph, because the specification, while being enabling for a nucleic acid encoding SEQ ID NO:2, does not reasonably provide enablement for Ftn2 genes or to nucleic acids that hybridize to an Ftn2 gene that encodes SEQ ID NO:2, vectors comprising it and cells, plants and seeds transformed with it. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention commensurate in scope with these claims.

The claims are broadly drawn to Ftn2 genes or to nucleic acids that hybridize to an Ftn2 gene that encodes SEQ ID NO:2, vectors comprising it and cells, plants and seeds transformed with it.

The instant specification, however, only provides guidance for isolation of Ftn2 from *Synechococcus* and identification of putative cynaobacterial homologs (examples 4 and 5), which has 17% identity to an unknown protein (SEQ ID NO:2, encoded by the genomic sequence SEQ

ID NO:3 and cDNA SEQ ID NO:2) in *Arabidopsis*; mapping the *arc6* mutation in *Arabidopsis* to show that it and the unknown protein map to chromosome 5 (example 2); rescuing the *arc6* mutation by SEQ ID NO:1 (example 2); analysis of the mutant to show that FtsZ rings and filaments are disrupted (example 2); identification of potential Ftn2 homologues from various database sequences (example 3); identification of arc5 (examples 6) and Fzo-like (example 7) genes from *Arabidopsis*. The specification teaches that Ftn2 does not have a proper DnaJ domain or a complete myb domain, but appears to have a chloroplast targeting sequence and three putative transmembrane helices (pg 90-91).

The instant specification fails to teach how to make nucleic acids that hybridize to a nucleic acid that encodes SEQ ID NO:2, wherein the nucleic acids encode AtFtn2 proteins.

The instant specification fails to provide guidance for which amino acids of SEQ ID NO:2 can be altered and to which other amino acids, and which amino acids must not be changed, to maintain Ftn2 activity of the encoded protein. The specification also fails to provide guidance for which amino acids can be deleted and which regions of the protein can tolerate insertions and still produce a functional enzyme.

Making "conservative" substitutions (*e.g.*, substituting one polar amino acid for another, or one acidic one for another) does not produce predictable results. Lazar et al (1988, Mol. Cell. Biol. 8:1247-1252) showed that the "conservative" substitution of glutamic acid for aspartic acid at position 47 reduced biological function of transforming growth factor alpha while "nonconservative" substitutions with alanine or asparagine had no effect (abstract). Similarly, Hill et al (1998, Biochem. Biophys. Res. Comm. 244:573-577) teach that when three histidines

that are maintained in ADP-glucose pyrophosphorylase across several species are substituted with the "nonconservative" amino acid glutamine, there is little effect on enzyme activity, while the substitution of one of those histidines with the "conservative" amino acid arginine drastically reduced enzyme activity (see Table 1). The nucleic acids encoding all these mutated proteins, however, would hybridize under high stringency to the nucleic acids encoding the original protein.

The only assay for FTN2 function is complementation of the arc6 mutation with a nucleic acid encoding SEQ ID NO:2 (exmaple2). It is not clear that other nucleic acids that hybridize to any nucleic acid that encodes SEQ ID NOL:2 would be able to complement this mutant, given the importance of individual amino acids in portion-protein interactions.

Given the claim breath, unpredictability, and lack of guidance as discussed above, undue experimentation would have been required by one skilled in the art to develop and evaluate Ftn2-encoding nucleic acids that hybridize to a nucleic acid that encodes SEQ ID NO:2. Making all possible single amino acid substitutions in an 801 amino acid long protein like that encoded by SEQ ID NO:1 and 3 would require making and analyzing 19^{801} nucleic acids; these proteins would have 99.8% identity to SEQ ID NO:2. Because nucleic acids that hybridize to a nucleic acid that encodes SEQ ID NO:2 would encode proteins with many amino acid substitutions, many more than 19^{801} nucleic acids would need to be made and analyzed. Guo et al (2004, Proc. Natl. Acad. Sci. USA 101: 9205-9210) teach that while proteins are fairly tolerant to mutations resulting in single amino acid changes, increasing the number of substitutions additively increases the probability that the protein will be inactivated (pg 9209, right column, paragraph

2). Thus, making and analyzing proteins with many amino acid substitutions that also have Ftn2 activity would require undue experimentation.

The specification does not teach how to use plants in which Ftn2 is overexpressed. The phenotype of such plants is not taught; thus one of skill in the art would not know how to use them.

As the specification does not describe the transformation of any plant with an Ftn2 gene or to a nucleic acid that hybridizes to an Ftn2 gene that encodes SEQ ID NO:2, undue trial and error experimentation would be required to screen through the myriad of nucleic acids encompassed by the claims and plants transformed therewith, to identify those with an unspecified phenotype.

Given the claim breath, unpredictability in the art, undue experimentation, and lack of guidance in the specification as discussed above, the instant invention is not enabled throughout the full scope of the claims.

8. Claims 1, 4-6 and 8-17 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter that was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention.

The essential feature of the claims is an Ftn2 gene or a nucleic acid that hybridizes to an Ftn2 gene that encodes SEQ ID NO:2. As the protein and its activity are novel, there is no well-developed field of prior art.

The specification describes FTN2 function as a protein that when its level are decreased leads to incomplete or no division of a prokaryote or plastid, resulting in long filamentous cells in cyanobacteria and single or few very large chloroplasts in plants (pg 15, lines 1-10).

The specification describes Ftn2 proteins as having a DnaJ-like domain at its N-terminal half, but that this domain is missing the essential central HPD motif (pg 60, lines 7-10; pg 90, lines 12-17). Otrer motifs are described (pg 60, lines 11-20; pg 90, lines 17-27; Table 7), but such motifs are not present in every protein indicated to be an Ftn2 homolog.

There is no description of the structure required for the recited function, and no description of the necessary and sufficient structural elements of a protein with Ftn2 function.

Furthermore, the specification describes no complete Ftn2 gene, with all its 5' and 3' regulatory elements.

The only species described in the specification is SEQ ID NOs:3 and 4, which encode SEQ ID NOs:2 and 5, respectively; these sequences do not include the complete regulatory elements of the genes. The putative homologs described in the specification are partial sequences whose function has not been determined.

One of skill in the art would not recognize that Applicant was in possession of the necessary common attributes or features of the genus in view of the disclosed species. Since the disclosure fails to describe the common attributes that identify members of the genus, and because the genus is highly variant, SEQ ID NOs:1 and 4 are insufficient to describe the claimed genus.

Hence, Applicant has not, in fact, described Ftn2 genes or nucleic acids that hybridize to an Ftn2 gene that encodes SEQ ID NO:2, and the specification fails to provide an adequate written description of the claimed invention.

Therefore, given the lack of written description in the specification with regard to the structural and functional characteristics of the claimed compositions, it is not clear that Applicant was in possession of the claimed genus at the time this application was filed.

9. The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

10. Claim 9 is rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter that Applicant regards as the invention. Dependent claims are included in all rejections.

Claim 9 lacks antecedent basis for the limitation "the organism".

Claim Rejections - 35 USC § 103

11. The following is a quotation of 35 U.S.C. 103(a), which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

12. Claim 1 is rejected under 35 U.S.C. 103(a) as being unpatentable over UniProt entry Q9FIG9 (2001, www.pir.uniprot.org/cgi-bin/upEntry?id=Q9FIG9).

The claims are drawn to a nucleic acid that hybridizes to a nucleic acid that encodes SEQ ID NO:2.

UniProt entry Q9FIG9 discloses the amino acid sequence of a protein with 99.8% identity to SEQ ID NO:2 (see search results). UniProt entry Q9FIG9 does not disclose a nucleic acid encoding the protein.

At the time the invention was made, it would have been obvious to one of ordinary skill in the art to derive a nucleic acid sequence encoding the protein taught by UniProt entry Q9FIG9. One of ordinary skill in the art would have been motivated to do so because of the established relationship in genetic code between nucleic acid and protein it encodes.

13. Claims 4-6 and 8-17 are free of the prior art, given the failure of the prior art to teach or suggest constructs comprising a nucleic acid that hybridizes to a nucleic acid that encodes SEQ ID NO:2, vectors comprising it and cells, plants and seeds transformed with it.

Conclusion

14. No claim is allowed.

15. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Anne R. Kubelik, whose telephone number is (571) 272-0801. The examiner can normally be reached Monday through Friday, 8:30 am - 5:00 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Anne Marie Grunberg, can be reached at (571) 272-0975.

The central fax number for official correspondence is (571) 273-8300.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to (571) 272-0547.

Patent applicants with problems or questions regarding electronic images that can be viewed in the Patent Application Information Retrieval system (PAIR) can now contact the USPTO's Patent Electronic Business Center (Patent EBC) for assistance. Representatives are available to answer your questions daily from 6 am to midnight (EST). The toll free number is (866) 217-9197. When calling please have your application serial or patent number, the type of document you are having an image problem with, the number of pages and the specific nature of the problem. The Patent Electronic Business Center will notify applicants of the resolution of the problem within 5-7 business days. Applicants can also check PAIR to confirm that the problem has been corrected. The USPTO's Patent Electronic Business Center is a complete service center supporting all patent business on the Internet. The USPTO's PAIR system provides Internet-based access to patent application status and history information. It also enables applicants to view the scanned images of their own application file folder(s) as well as general patent information available to the public.

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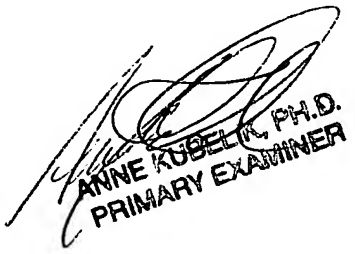
Anne Kubelik, Ph.D.
February 24, 2006



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RA Osteryoung K.W.;
RT "ARC6 is a J-domain plastid division protein and an evolutionary
RT descendant of the cyanobacterial cell division protein Ftn2.";
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Qy        781 RYEVFWSKSGWKITEGSVLAS 801
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Db        781 RYEVFWSKSGWKITEGSVLAS 801
```

RESULT 3
Q9FIG9
ID Q9FIG9 PRELIMINARY; PRT; 801 AA.
AC Q9FIG9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MDH9
DE (Hypothetical protein At5g42480).
GN Name=At5g42480;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99156233; PubMed=10048488;
RA Asamizu E., Sato S., Kaneko T., Nakamura Y., Kotani H., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VIII.
RT Sequence features of the regions of 1,081,958 bp covered by seventeen
RT physically assigned P1 and TAC clones.";
RL DNA Res. 5:379-391(1998).
RN [2]
RP SEQUENCE FROM N.A.

```
RA   Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
RA   Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
RA   Tang C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bowser L.,
RA   Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA   Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA   Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA   Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Shinozaki K.,
RA   Davis R.W., Ecker J.R., Theologis A.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA   Quach H.L., Tang C., Toriumi M., Wallender E.K., Wong C., Wu H.C.,
RA   Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA   Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA   Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA   Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA   Theologis A.;
RL   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB016888; BAB10489.1; -.
DR   EMBL; AY091075; AAM13895.1; -.
DR   EMBL; AY150490; AAN12907.1; -.
DR   InterPro; IPR001623; DnaJ_N.
KW   Hypothetical protein.
SQ   SEQUENCE   801 AA;  88259 MW;  608E776FBA73FECF CRC64;

  Query Match             99.7%;  Score 4051;  DB 2;  Length 801;
  Best Local Similarity   99.8%;  Pred. No. 3.8e-240;
  Matches  799;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MEALSHVGIGLSPFQLCRLPPATTKLRRSHNTSTTICSASKWADRLLSDFNFTSDSSSSS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEALSHVGIGLSPFQLCRLPPATTKLRRSHNTSTTICSASKWADRLLSDFNFTSDSSSSS 60

Qy         61 FATATTTATLVSLPPSIDRPERHVPIPIDFYQVLGAQTHFLTDGIRRAFEARVSKPPQFG 120
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FATATTTATLVSPPPSIDRPERHVPIPIDFYQVLGAQTHFLTDGIRRAFEARVSKPPQFG 120

Qy        121 FSDDALISRRQILQAACETLSNPRSRREYNEGLLDDEEATVITDVPWDKVPGALCVLQEG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 FSDDALISRRQILQAACETLSNPRSRREYNEGLLDDEEATVITDVPWDKVPGALCVLQEG 180

Qy        181 GETEIVLRVGEALLKERLPKSFKQDVVLVMALAFLDVSRDAMALDPPDFITGYEFVEEAL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GETEIVLRVGEALLKERLPKSFKQDVVLVMALAFLDVSRDAMALDPPDFITGYEFVEEAL 240

Qy        241 KLLQEEGASSLAPDLRAQIDETLEEITPRYVLELLGLPLGDDYAAKRLNGLSGVRNILWS 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 KLLQEEGASSLAPDLRAQIDETLEEITPRYVLELLGLPLGDDYAAKRLNGLSGVRNILWS 300

Qy        301 VGGGGASALVGGLTREKFMNEAFLRMTAAEQVDLFVATPSNIPAESFEVYEVALALVAQA 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 VGGGGASALVGGLTREKFMNEAFLRMTAAEQVDLFVATPSNIPAESFEVYEVALALVAQA 360

Qy        361 FIGKKPHLLQDADKQFQQLQQAKVMAMEIPAMLYDTRNNWEIDFGLERGLCALLIGKVDE 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 FIGKKPHLLQDADKQFQQLQQAKVMAMEIPAMLYDTRNNWEIDFGLERGLCALLIGKVDE 420

Qy        421 CRMWLGLDSEDSQYRNPAIVEFVLENSNRDDNDDLPGLCKLLETWLAGVVFPRFRDTKDK 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CRMWLGLDSEDSQYRNPAIVEFVLENSNRDDNDDLPGLCKLLETWLAGVVFPRFRDTKDK 480

Qy        481 KFKLGDYYDDPMVLSYLERVEVVQGSPLAAAATMARIGAEHVKASAMQALQKVFPSRYTD 540
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        481 KFKLGDYYDDPMVLSYLERVEVVQGSPLAAAAAMARIGAEHVKASAMQALQKVFPSRYTD 540

Qy        541 RNSAEPKDVQETVFSVDPVGNNVGRDGEPGVFIAEAVRPSENFETNDYAIRAGVSESSVD 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 RNSAEPKDVQETVFSVDPVGNNVGRDGEPGVFIAEAVRPSENFETNDYAIRAGVSESSVD 600

Qy        601 ETTVEMSVADMLKEASVKILAAGVAIGLISLFSQKYFLKSSSSFQRKDMVSSMESDVATI 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ETTVEMSVADMLKEASVKILAAGVAIGLISLFSQKYFLKSSSSFQRKDMVSSMESDVATI 660

Qy        661 GSVRADDSEALPRMDARTAENIVSKWQKIKSLAFGPDHRIEMLPEVLDGRMLKIWTDRAA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GSVRADDSEALPRMDARTAENIVSKWQKIKSLAFGPDHRIEMLPEVLDGRMLKIWTDRAA 720

Qy        721 ETAQLGLVYDYTLLKLSVDSVTVSADGTRALVEATLEESACLSDLVHPENNATDVRTYTT 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ETAQLGLVYDYTLLKLSVDSVTVSADGTRALVEATLEESACLSDLVHPENNATDVRTYTT 780

Qy        781 RYEVFWSKSGWKITEGSVLAS 801
              |||||||||||||||||||||
Db        781 RYEVFWSKSGWKITEGSVLAS 801


RESULT 4
Q6Z729
ID   Q6Z729      PRELIMINARY;      PRT;   760 AA.
AC   Q6Z729;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Plastid division protein.
GN   Name=P0575F10.2;
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RT   "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, PAC
RT   clone:P0575F10.";
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AP004885; BAD07942.1; -.
DR   InterPro; IPR001623; DnaJ_N.
SQ   SEQUENCE   760 AA;  84134 MW;  2C446848627958B2F CRC64;

  Query Match             43.7%;  Score 1775.5;  DB 2;  Length 760;
  Best Local Similarity   47.9%;  Pred. No. 2.1e-100;
  Matches  390;  Conservative  119;  Mismatches  213;  Indels   93;  Gaps   16;

Qy         12 SPFQLCRLPPATTKLRRSHNTSTTIC-SASKWADRLLSDFNF-----TSDSSSSSPATAT 65
              :||       |      ||      :  | :||:||:|| :||:        ||  | : | |
Db         14 APFAFSLPRPRPRPRRRPPPHPSAACRAASRWAERLFADFHLLPTAAPSDPPSPAPAPAA 73

Qy         66 TTATLVSLPPSIDRPERHVPIPIDFYQVLGAQTHFLTDGIRRAFEARVSKPPQFGFSDDA 125
              :   :|   |  || :|: :|||:||||: ||| ||||||||||:|||||:|:| ||
Db         74 APSASPFVPLFPDAAERSLPLQVDFYKVLGAEPHFLGDGIRRAFEARIAKPPQYGYSTDA 133

Qy        126 LISRRQILQAACETLSNPRSRREYNEGLLDDEEATVITDVPWDKVPGALCVLQEGGETEI 185
              |: |||:|| | :|| |  || :|:  | :: |  :  |: |||         | ||
Db        134 LVGRRQMLQIAHDTLMNQNSRTQYDRALSENREEALTMDIAWDK---------EAGEALA 184

Qy        186 VLRVGEALLKERLPKSFKQDVVLVMALAFLDVSRDAMALDPPDFITGYEFVEEALKLLQE 245
              ||  || || :| || ||||||| ||||::|:|||||  ||| |   | :| |||||||
Db        185 VLVTGEQLLLDRPPKRFKQDVVLAMALAYVDLSRDAMAASPPDVIGCCEVLERALKLLQE 244

Qy        246 EGASSLAPDLRAQIDETLEEITPRYVLELLGLPLGDDYAAKRLNGLSGVRNILWSVGGGG 305
              :|||:||||| :|||||||||||| ||||| ||:  ::  ||  || | |||||||| ||
Db        245 DGASNLAPDLLSQIDETLEEITPRCVLELLSLPIDTEHHKKRQEGLQGARNILWSVGRGG 304

Qy        306 ASALVGGLTREKFMNEAFLRMTAAEQVDLFVATPSNIPAESFEVYEVALALVAQAFIGKK 365
              : : || :|| |||||||||: ||:| |  ||::|| | ||:| |||| |||| | |:
Db        305 IATVGGGFSREAFMNEAFLRMTSIEQMDFFSKTPNSIPPEWFEIYNVALAHVAQAIISKR 364

Qy        366 PHLLQDADKQFQQLQQAKVMAMEIPAMLYDTRNNWEIDFGLERGLCALLIGKVDECRMWL 425
              |  :  ||  |:|||:  : :       ||      |:|  |||  |:||:| | :|||||
Db        365 PQFIMMADDLFEQLQKFNIGS----HYAYDN----EMDLALERAFCSLLVGDVSKCRMWL 416

Qy        426 GLDSEDSQYRNPAIVEFVLENSN-RDDNDDLPGLCKLLETWLAGVVFPRFRDTKDKKFKL 484
              |:|:| | ||:| |:||:: ||:  ::|| ||||||||||||   |||| |||:  :|:|
Db        417 GIDNESSPYRDPKILEFIVTNSSISEENDLLPGLCKLLETWLIFEVFPRSRDTRGMQFRL 476
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